

Figure 1  
(Sheet 1 of 17)

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MOTTOESCHGEPUTEDGWELJLCRGEINPGCEGKKKGKFKVKVFSSEVAPEVLFILLITFWHLPAPNLVVS1VGEERPLAMKSWLRDVLF  
KGLVKHAQSTGAWILTEALHVGLAHHVGCAVHDHSLAESTTKIRVVAJGMASLDFJ1HKQ1LDGVHOKEDTPJHYPADEGNJQGPLCP1  
DENLSEHF11VEFGALGSGNDG1TE1Q1S1EKKHJSQORTCGGGTSC1Q1FVLCLLVNGDPNTLER1SRAVEQAAPW1LAGSGGIADVLA  
ALVSGPHLLVHQVAKOFREKFFSECFSWEAJVHWTELLQNJAAH1HLLTVYDFEQECS1DLDTV1LKA1VKACKSHSQAQDYLDELY  
LAVAWDKVIJAKSEJFNGDVWKS1D11EVMDALVENKFDFVRLFVDSGADMALFLTYGRLOCLYHSVSFKSLLFELLORKHEEGRLT  
L4GLGAQCAK1P1GL1AFSLHVS1V1KDF1HDAC1GFYQDGRKMEERGI1KK12GOKWLFD1SKSEDPWDLFLWAVLQNYEMATY  
EWAJMGREGVAA1A1ACKJ1KEMSHLEKEAEVAK1MREAKYEQ1ALD1FSECYGNSEEDRAFALLV1RNHEWSRTTCLHATEADAKAFFA  
EDCVQCAF1TKJWWGLM1TGTP1L111GAFTCAL1YTNIJSFSEDAPQ1MDLED1QEPD1DMEKS11CSF1CSPCGQOLEKLTEAPAPGDLG  
1QAAFL1TRWKKFWGAFTVFLGNVVMY1AFLFLFTYVLLVDFR1F1PQG1SCSEVTLYFWVFT1VLE1BQGFTDEDTHLVKKFTLYV  
EDNWNC1DMVA1FLF1VGVTCKMVP1VFLAGRTVLA1DFMVFT1K1J1FA1HKQ1LGFK111VERMMKDVF1FLF1SVWLVAYGVTT  
A1LHFHDGKLEW1F1R1VLYAFYLO1FGQ1FLDE1DEARVNCS1HPL1LES1ASC1F1LY1ANW1V11LLVTFL1VTNV1LMN111AMFSY1  
F1VVOQNAADM1WKFQ1YH11VEYHGR1A1FF111S1H1S1V1KQV1R1KEA1H1K1QH1ER1LFD1DQK111TWETVQKENF1STMEK1  
E1SEGEV1R1KTAH1V11AKY1JGLRE1EKK1K1LES1ANYCML111SM1D1LAPGGTY111SONCGCR1S1Q1A1DREY1LES1GLPPSDT

Figure 2  
(Sheet 2 of 17)  
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Human TFR<sub>1</sub> nucleotide sequence

SEQ New: 3498 bp

Composition: 634 A; 1089 C; 1143 G; 632 T; 0 OTHER

Percentage: 18% A; 31% C; 33% G; 18% T; 0% OTHER

Molecular weight (kDa): ssDNA: 1081.34 dsDNA: 2157.1

ORIGIN

1 ATGCAGGATG TCCAAGGCC CGTCCCCGGA AGCCCCGGG ATGCTGAAGA CGGGCGGGAC  
61 C1GGGCTTGC ACAGGGGGCGA GGTCAACTT GGAGGGTCTG GGAAGAAGCG AGGCAAGTT  
121 GTACGGCTGC CGAGCGGAGT GGGCCCGCT GTGCTCTTTC ACCTGCTGCT TGCTGAGTGG  
181 CACCTGCCGG CCCCCAACCT GGTGGTGTCC CTGGTGGGTG AGGAGCAGCC TTTGCCATG  
241 AAATCCGGC TCGGGATGT GCTGCCAAG GGGCTGGTCA AGGCAGCTCA GAGCACAGGA  
301 GCCTGATCC TGACCACTGC CCTCCCGCTG GGCGCTGGCCAG GGCATGTCGG GCAGGCCGTC  
361 CGCGACCACT CGCTGGCCAG CACGTCCACC AAGGTCCCTG TGTTGCTGT CGGCATGGC  
421 TCGCTCCGCC GCCTCCTGCA CGGCCFCATT CTGGAGGAGG CCCAGGAGGA TTTTCCGTG  
481 CACTACCCCTG AGGATGACGG CGGCAGCCAG GGCCCCCTCT GTTCACTGGA CAGCAACCTC  
541 TCCCACCTCA TCCCTGGTGGA GCCAGGGCCC CGGGGGAGG GCGATGGCT GACGGAGCTC  
601 CGGGCTGAGGC TGGAGAAGCA CATCTGGAG CAGAGGGCGG GCTACGGGG CACTGGCAGC  
661 ATCGAGATCC CTGTCCTCTG CTTGCTGGTC AATGGTGTATC CCAACACCTT GGAGAGGATC  
721 TCCAGGGCCG TGGAGCAGGC TGCCCCGTGG CTGATCCTGG TAGGCTCGGG GGGCATCGCC  
781 GATGTCTTG CTGCCCTAGT GAAACAGCCC CACCTCTGG TGCCCCAAGCT GGGCGAGAAC  
841 CACTTTAGG AGAAGTCCCC CAGCAAGCAI TTCTCTTGGG AGGACATCGT GCGCTGGAC  
901 AAGCTCTGC AGAACATCAC CTCACACCCAG CACCTGCTCA CCGTGTATGA CTTCGAGCAG  
961 GAGGGCTCCG AGGAGCTGGA CACGGTCATC CTGAAGGCGC TGGTAAAGC CTGCAAGAGC  
1021 CACAGCCAGG AGCCTCAGGA CTATCTGGAT GAGCTCAAGC TGGCCGTGGC CTGGGACCGC  
1081 GTGGACATCG CCAAGAGTGA GATCTTCAI GGGGACGTGG AGTGGAAAGTC CTGTGACCTG  
1141 GAGGAGGTGA TGGTGGACGC CCTGGTCAGC AACAAAGCCCG AGTTTGTGCG CCTCTTTGTG  
1201 GACACCGCC CAGACGTGGC CGACTTCTG ACCTATGGGC GGCTGCAGGA GCTCTACCGC  
1261 TCCCTGTCAC GCAAGAGCC GCTCTTCGAC CTGCTGCAGC GGAAGCAGGA GGAGGCCC  
1321 CTGACGCTGG CGGGCCTGGG CACCCAGCAG GCCCGGGAGC CACCCCGGGG GCCACCGGGC  
1381 TTCTCCCTGC ACGAGGTCTC CGCGTACTC AAGGACTTCC TGCAGGACGC CTGCGAGGC  
1441 TTCTACCAAGG ACGGCCGGCC AGGGGACCGC AGGAGGGCGG AGAAGGGCCC GGCCAAGC  
1501 CCCACGGGCC AGAAGTGGCT GCTGGACCTG AACCAAGAAGA GCGAGAACCC CTGGCGGGAC  
1561 CTETTCTGT GGGCCGTGCT GCAGAACCGC CACGAGATGG CCACCTACTT CTGGGCCATC  
1621 GGCCAGGAAG GTGTGGCAGC CGCACTGGCC GCCTGAAAA TCCTCAAAGA GATGTGCGCAC  
1681 CTGGAGACGG AGGCGCAGGC GGCCCCAGCC ACGGCGGAGG CGAAATACGA GCGGCTGGCC  
1741 CTTGACCTCT TCTCCGAGTG CTACAGCAAC AGTGAGGCC GCGCCTTCGC CCTGCTGGT  
1801 CGCCCGAACCC GCTGCTGGAG CAAGACCACC TGCTGCACC TGGCCACCGA GGCTGACGCC  
1861 AAGGCCCTCT TTGCCCCAGA CGGCGTTCAG GCCTTCTGA CCAGGATCTG GTGGGGGGAC  
1921 ATGGCCCGAG GCACGCCCAT CCTGCGGCTG CTAGGAGCCT TCCTCTGCC CGCCCTCGTC  
1981 TATACCAACC TCATCACCTT CAGTGAGGAA GCTCCCCCTGA GGACAGGCCT GGAGGACCTG  
2041 CAGGACCTGG ACAGCCTGGA CACGGAGAAG AGCCCGCTGT ATGGCCTGCA GAGCCGGGTG  
2101 GAGGGAGCTGG TGGAGGCGCC GAGGGCTCAG GGTGACCGAG GCCCACGTGC TGTCTTCTG  
2161 CTCACACGCT GGGGAAATT CTGGGGCCT CCCGTACTG TGTTCTGGG GAACTGGTC  
2221 ATGTACTTCG CCTTCCTCTT CCTGTCACC TACGTCCTGC TGTTGGACTT CAGGCCGCC  
2281 CCCCCAGGGGCC CCTCAGGGCC CGAGGTCACT CTCTACTTCT GGGTCTTTAC GCTGGTGTG  
2341 GAGGAATCC GGCAGGGCTT CTTCACAGAC GAGGACACAC ACCTGGTGAA GAAAGTCA  
2401 CTGTATGTGG GGGACAACCTG GAAACAAGTGT GACATGGTGG CCATCTTCCT GTTCATCGTC  
2461 GGTGTACACT GCAGGATGCT GCCGTCGGCG TTGAGGCTG GCGCACGGT CCTCGCCATC  
2521 GACTTCATGG TGTTCACGCT GCGGCTGATC CATATCTTG CCATACACAA GCAGCTGGGC  
2581 CCCAAGATCA TCGTGGTAGA GCGCATGATG AAGGACGTCT TCTTCTTCCT CTTCTTCTG  
2641 AGCGTGTGGC TCGTGGCCTA CGGTGTCACC ACCCAGGCGC TGCTGCACCC CCATGACGGC  
2701 CGCCTGGAGT GGATCTTCCG CGGGGTGCTC TACCGGCCCT ACCTGCAGAT CTTCGGCCAG  
2761 ATCCCACCTGG ACGAGATGTA TGAAGCCCGT GTGAACCTGCT CCACCCACCC ACTGCTGCTG  
2821 GAGGAACCTCAC CATCCTGCC CAGCCTCTAT GCCAACGTGC TGGTCATCCT CCTGCTGGTC  
2881 ACCTTCTGT TGGTCAACCAA TGTGCTGCTG ATGAACCTGC TCATCGCCAT GTTCAGCTAC  
2941 ACGTCCAGG TGGTGCAGGG CAACGCAGAC ATGTTCTGGA AGTTCCAGCG CTACAACCTG

Figure 3A  
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301 ATTCTGGAGT ACCACGAGCG CCCCCGCCCTG GCCCCCGCCCT TCATCCCTGCT CAGCCACCTG  
302 AGCCCTGACGC TCCGCCGGGT CTTCAGAGAG GAGGCTGAGC ACAAGCGGGGA GCACCTGGAG  
303 AGAGACCTGG CAGACCCCCC GAGACAGAG GTCCTCACCT GGGAGACAGT CCAGAGAGGAG  
304 AACTTCTGAA GCAAGATGGA GAAAGCCGAGG AGCAGACGCC AGGGGGAGGT GCTGCGGAA  
305 ACCGCCACAA GAGTGGACTT CATTGCCAAC TACCTCTGGG GGCTGAGAGA GCAAGAAAAAC  
306 CGCATCAAGT GTCTGAGTC ACAGATCAAC TACTGCCCGG TGCTCGTGTGTC CTCCGTGGCT  
307 GACGTGCTGG CCCAGGGTGG CGGCCCCCGG AGCCTCTCAGC ACTGTGGCGA GGGAGGCCAC  
308 CTGGTGGCTG CTGACCACAG AGGTGGTTA GATGGCTGGG AACAAACCGG GGCTGGCCAG  
309 CCTCCCTCGG ACACATGA

Figure 3B  
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Human CFF8 protein coding sequence  
Translational of Htrpb coding (1-3498)  
Universal code  
Octet amino acid number: 1165, MW=13128.  
Max ORF: 1-3495, 1165 AA, MW=13128.

ORIGIN

1 MCDVQGPRPG SPGDAELARE LGLHFGEVNF GGSGKKRGKF VRVPSGVAPS  
2 VLFDLILLAEW HLFAPNLVVS LVGEEQFFAM KSWLDRVLRK GLVKAAQSTG  
3 AWIILTSALRV GLARHVGQAV FDHCLASTST KVRVVAVGMA SLGRVLHRRK  
4 LEEAQEDFPV HYPEDDGGSQ GPLCSLDSNL SHFILVEPGP PGKGDGLTEL  
5 FLRLEKKHISE QFAGYGGTGS JEIFVLCILV NGDPNTLERJ SRAVEQAAAPW  
6 LILVGSGGIA DVLAALVNQF HLLVPKVAEK QFKEKFPSKH FSWEDIVRWI  
7 FLLQNIITSHQ HLLTVYDFE $\varphi$  LGSEELDTVJ LKALVKACKS HSQEPQDYLI  
8 ELKLAVALWDR VDIAKSEJFN GDVEWKSCDL EEVVMVDALVS NKPEFVRLFV  
9 DNGADVADFI TYGRLQELYR SVSRKSELLFD LLQRKQEEAR LTLAGLGTQ $\varphi$   
10 AREPPFAGFFA FSLHEVSRVL KDFLQDACRG FYQDGRPGDR RRAEKGPAKK  
11 FTGOKWILDL NQKSENFWRD LFLWAVLQNF HEMATYFWAM GQEGVAAALA  
12 ACKILKEMSH LETEAEAAARA TREAKYERLA LDLFSECYSN SEARAFALLV  
13 RANRCWSKTT CLHLATEADA KAFFAHDGVQ AFLTRIWWGD MAAAGTPILRI  
14 LGAFLCFLALV YTNLITFSEE AFLKTGLEDL QDLDSDLTEK SPLYGLQSRV  
15 EELVEAPRAQ GDRGPRAVFL LTRWRKFVWGA PVTVFLGNVV MYFAFLFLFT  
16 YVLLVDFRPP POGPSGFEST 1YFWVFTLVL EEIIRQGFFTD EDTHLVKKFT  
17 LYVGDNWNKC DMVAJFLFIV GVTCKMLPSA FEAGRTVLM DFMVFTLRLI  
18 H1FAJHKQLG PK11VVERMM KDVFFFLLFFL SVWLVAYGVT TOALLHPHDG  
19 F1EWFRRVL YRPYLQ1FGQ JPLDEJDEAR VNCSTHPLLL EDSPSCPSLY  
20 ANWLWJ1LLV TFL1LVTNVLL MNLLJAMFSY TFOVVOGNAD MFWKFORYNL  
21 IVEYHERP $\varphi$  AL APPF1LLSHL S1T1RRVFKK EAEHKREHLE RDLPDPPLDOK  
22 VVTWETVOKE NFLSKMEKRR RDSEGEVLRK TAHRVDFIAK YLGGLREQEK  
23 F1KCLESQIN YCSVLVESVA DVLAQGGGPK SSQHCGEGSQ LVAADHKG $\varphi$   
24 DGWEQPGAGQ PPSDT\*

Figure 4  
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FIGURE 5 - Comparison of the amino acid sequences of mouse and human TRP1

mTRP1	MOTTCQESCTGSIIDENWELLICFGIINFGCSCRFKFWVVPSSVAFPSVLFEILLITEW 60
hTRP1	MCDEVQFRKPCSGPGLAILRFEICLHLHGEVNIQCSGKRFKFWVPSGVAPSVLFDLLLAEW 60
mTRP1	*** . . . *** . . . *** :***** . . . *** . . . *** :*** :***
hTRP1	*** . . . *** . . . *** :***** . . . *** . . . *** :*** :***
mTRP1	HLIFAPNLVVSINGELHILAMKSWLRLVIRGIVHLACSTGAWIILTSALHVGLARHVGCAY 120
hTRP1	HLIFAPNLVVSINGELHILAMKSWLRLVIRGIVHLACSTGAWIILTSALHVGLARHVGCAY 120
mTRP1	*** . . . *** . . . *** :***** . . . *** . . . *** :*** :***
hTRP1	*** . . . *** . . . *** :***** . . . *** . . . *** :*** :***
mTRP1	REHSLASTSTKIVVVAICMGLSLEDFILHRCCLINGVHORLDTPIHYFADEGNIQGFLCPLDS 180
hTRP1	REHSLASTSTKIVVVAICMGLSLEDFILHRCCLINGVHORLDTPIHYFADEGNIQGFLCPLDS 180
mTRP1	*** . . . *** . . . *** :*** :*** : . . . *** . . . *** . . . ***
hTRP1	*** . . . *** . . . *** :*** :*** : . . . *** . . . *** . . . ***
mTRP1	NLSHFIILVESGAIQSGNDGLTELQLSLEKHSQGFTGIGGTSC1QIPVLCLLVNNGDPNTL 240
hTRP1	NLSHFIILVESGAIQSGNDGLTELQLSLEKHSQGFTGIGGTSC1QIPVLCLLVNNGDPNTL 240
mTRP1	*** . . . *** . . . *** :*** :*** : . . . *** . . . *** . . . ***
hTRP1	*** . . . *** . . . *** :*** :*** : . . . *** . . . *** . . . ***
mTRP1	ERISRAVEQAAPIIILAGSGGIADVIAALVSC1H11VFOVAEKOFREKFPSECFSWEAIV 300
hTRP1	ERISRAVEQAAPIIILAGSGGIADVIAALVNC1H11VFOVAEKOFREKFPSECFSWEAIV 300
mTRP1	*** . . . *** . . . *** :*** :*** : . . . *** . . . *** . . . ***
hTRP1	*** . . . *** . . . *** :*** :*** : . . . *** . . . *** . . . ***
mTRP1	HWTEILLONIAAHFHLLTVYDFEQEGSEELDTVILKALVKACKSHSQEADQYLDDELKLAVA 360
hTRP1	HWTEILLONITSHOHLLTVYDFEQEGSEELDTVILKALVKACKSHSQEADQYLDDELKLAVA 360
mTRP1	*** . . . *** :*** :*** : . . . *** . . . *** . . . *** . . . ***
hTRP1	*** . . . *** :*** :*** : . . . *** . . . *** . . . *** . . . ***
mTRP1	WDFVDIAKSEIFNGDVEWKSCDLEEVMTDAIVSNHDFVRLFVDSGADMADFLLTYGRLOQ 420
hTRP1	WDFVDIAKSLIFNGDVEWKSCDLEEVMTDAIVSNHDFVRLFVDSGADMADFLLTYGRLOQ 420
mTRP1	*** . . . *** . . . *** :*** :*** : . . . *** . . . *** . . . ***
hTRP1	*** . . . *** . . . *** :*** :*** : . . . *** . . . *** . . . ***
mTRP1	LYHEVSFKSLLFELLQKHEEGRITLAGLGAQQKARELFIGLFAFSLHEVSRVLKDFLHDA 480
hTRP1	LYRSVFKSLLFELLQKHEEGRITLAGLGAQQKARELFIGLFAFSLHEVSRVLKDFLHDA 480
mTRP1	*** . . . *** :*** :*** : . . . *** . . . *** . . . *** . . . ***
hTRP1	*** . . . *** :*** :*** : . . . *** . . . *** . . . *** . . . ***
mTRP1	CRGFYQDGK---RMEERGFKRFAGQKWLFLSLMSEDPWRDLFLWAVLQNRYEMATYF 536
hTRP1	CRGFYQDGKPGDKKAERGFAKRPTGQKWLFLDNLQKSENPWRDLFLWAVLQNRYEMATYF 536
mTRP1	*** . . . *** :*** :*** : . . . *** . . . *** . . . *** . . . ***
hTRP1	*** . . . *** :*** :*** : . . . *** . . . *** . . . *** . . . ***
mTRP1	WAMGREGVAAALAAACKIJKEMSHLEKEAELAATMREAKYEQLALDLFSECYGNSEDRADA 596
hTRP1	WAMGQEGVAAALAAACKIJKEMSHLETEAAKATREAKYERLALDLFSECYNSEARADA 597
mTRP1	*** . . . *** :*** :*** : . . . *** . . . *** . . . *** . . . ***
hTRP1	*** . . . *** :*** :*** : . . . *** . . . *** . . . *** . . . ***

Figure 5  
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Classification and Secondary Structure Prediction of Membrane Protein

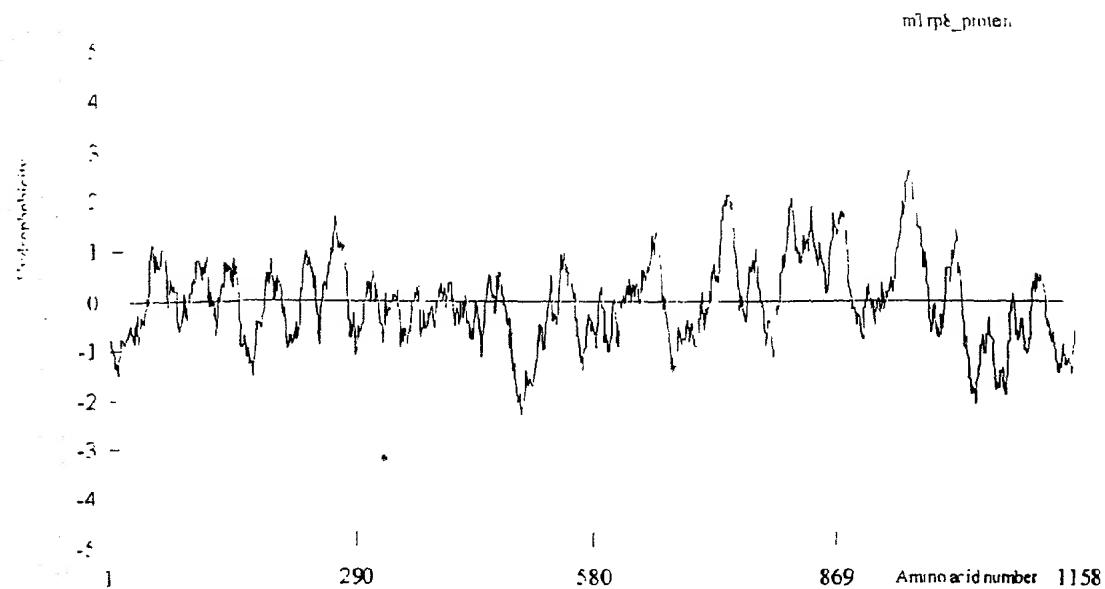
<http://azur.ejp.riken.ac.jp/sosui/>

Orientation c: the N-terminus of mTrp8: 11  
Number of transmembrane helices of mTrp8: 6  
Position of transmembrane helices of mTrp8: helix begin end  
1 731 751  
2 769 791  
3 807 829  
4 834 861  
5 870 893  
6 951 971

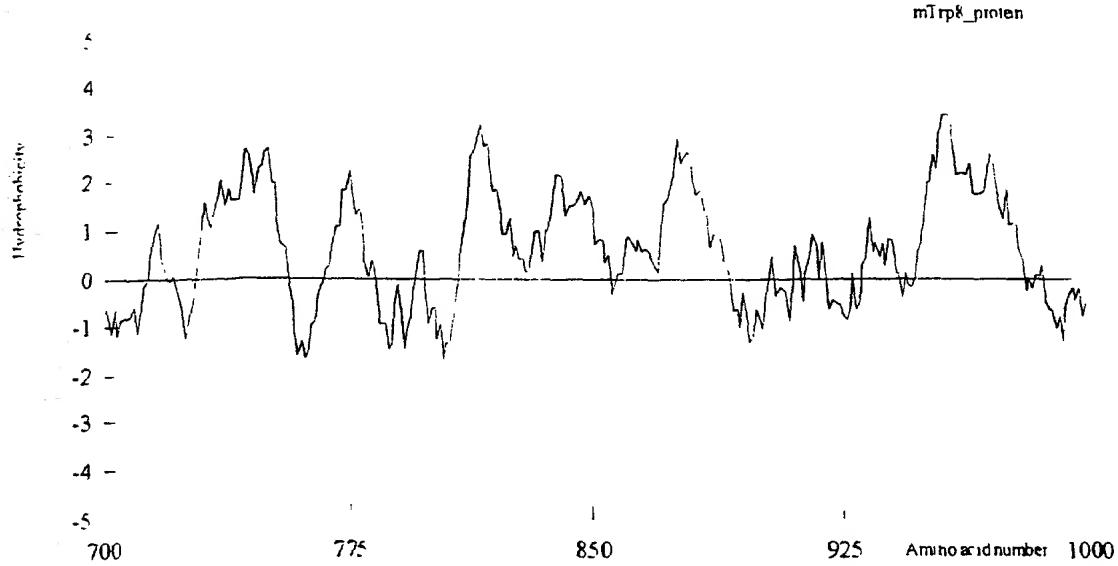
Orientation c: the N-terminus of hTrp8: 1K  
Number of transmembrane helices of hTrp8: 6  
Position of transmembrane helices of hTrp8: helix begin end  
1 733 751  
2 770 791  
3 807 829  
4 843 863  
5 871 893  
6 951 971

Figure 6A  
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Hydrophobicity profile of mTrp<sup>K</sup> made with DNAMAN software



mTrp<sup>K</sup>\_protein



mTrp<sup>K</sup>\_protein

Figure 6B  
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Hydrophobicity profile of hTrpE (Made with DNAMAN software)

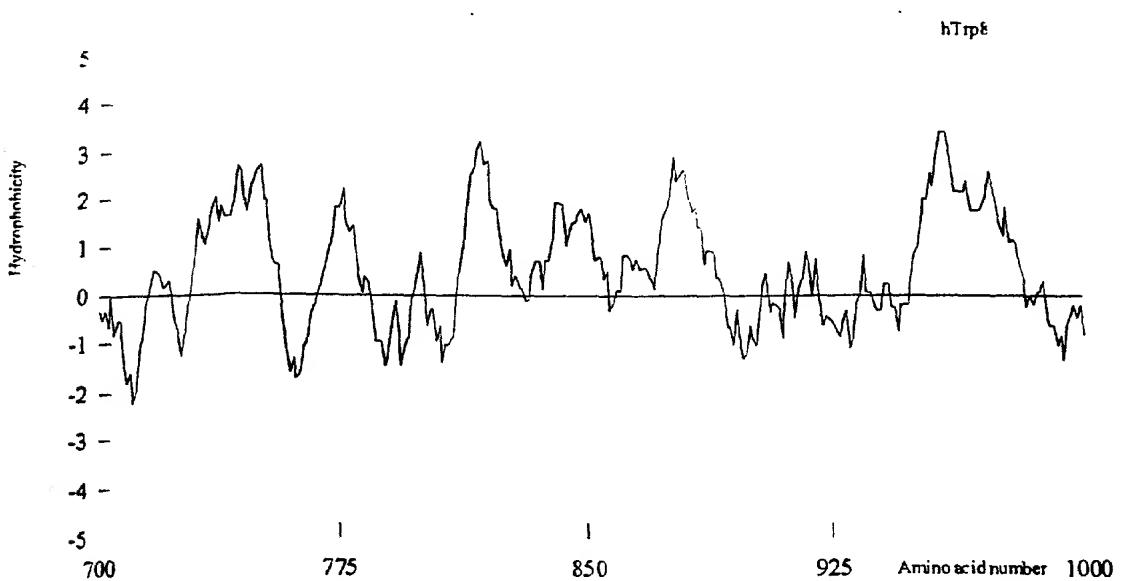
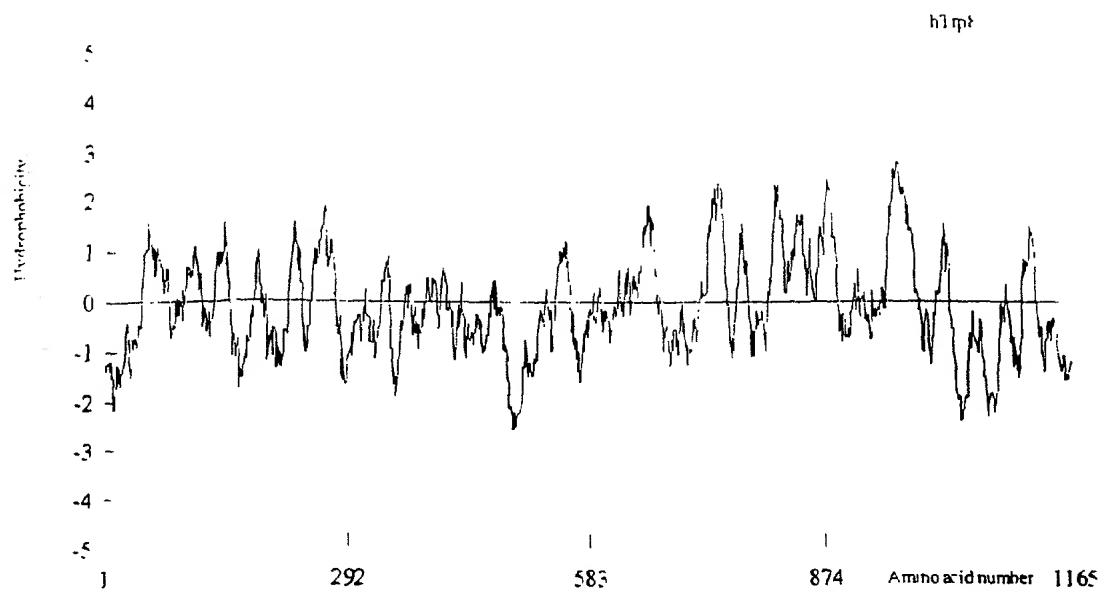


Figure 6C  
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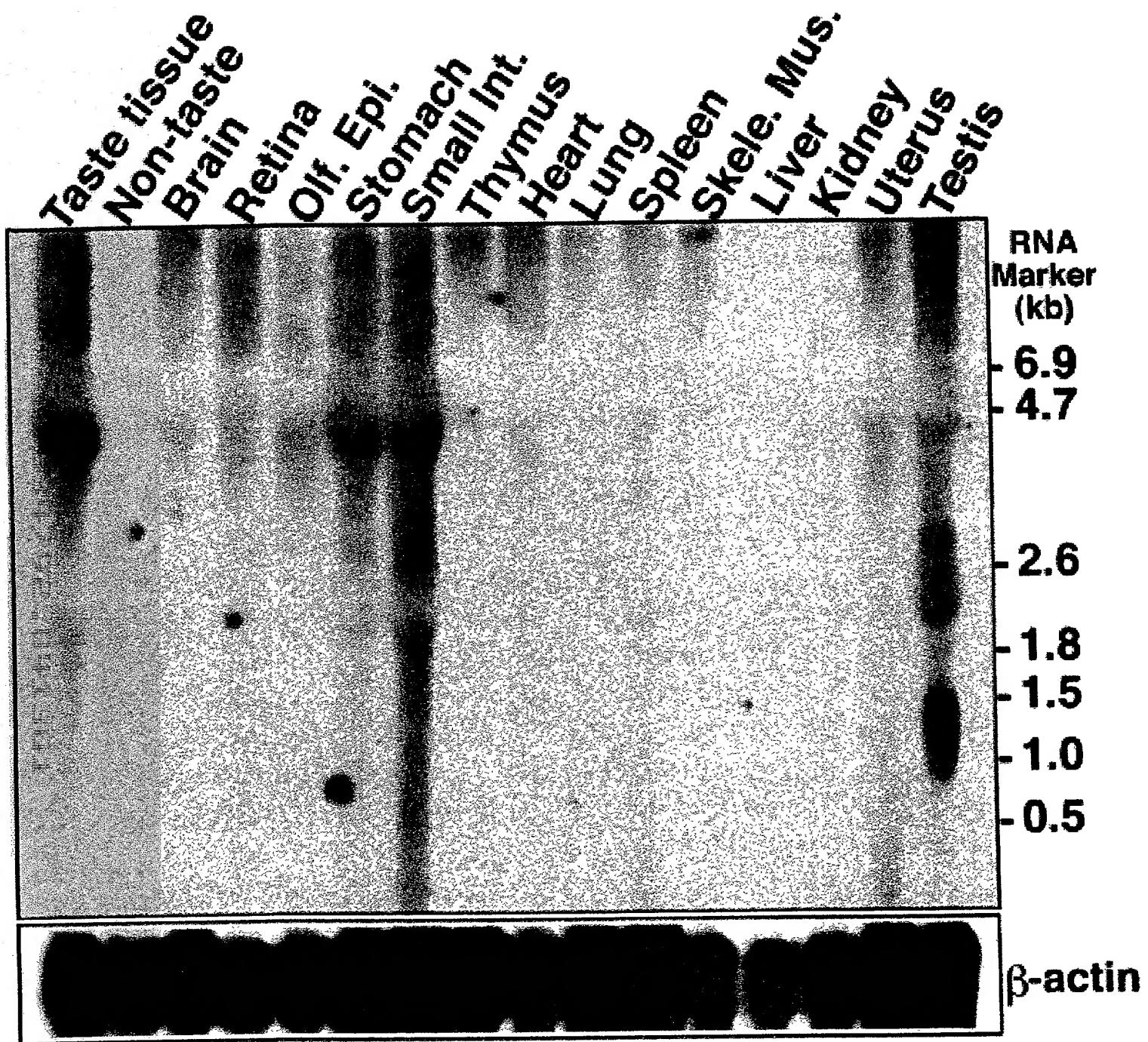


Figure 7  
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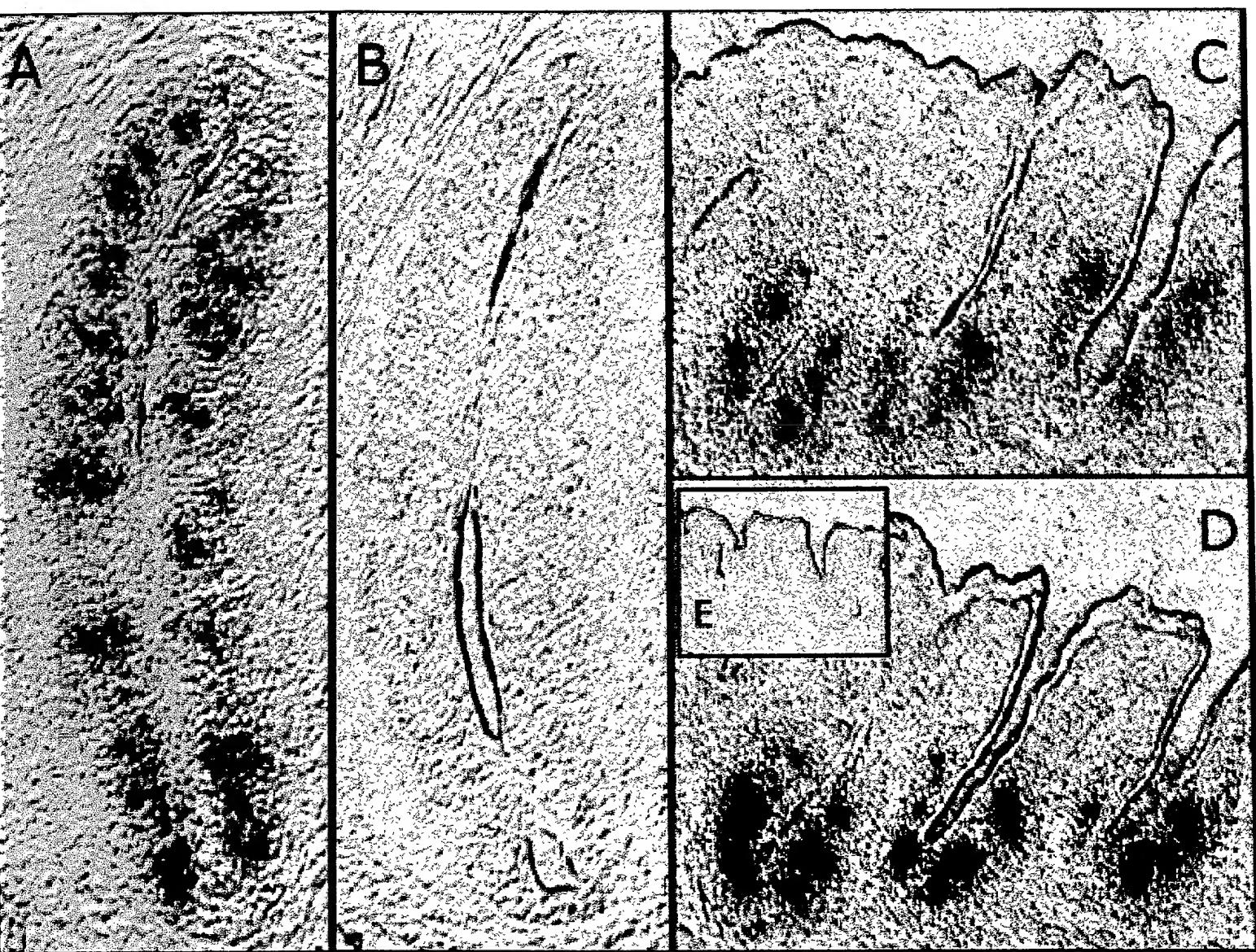


Figure 8  
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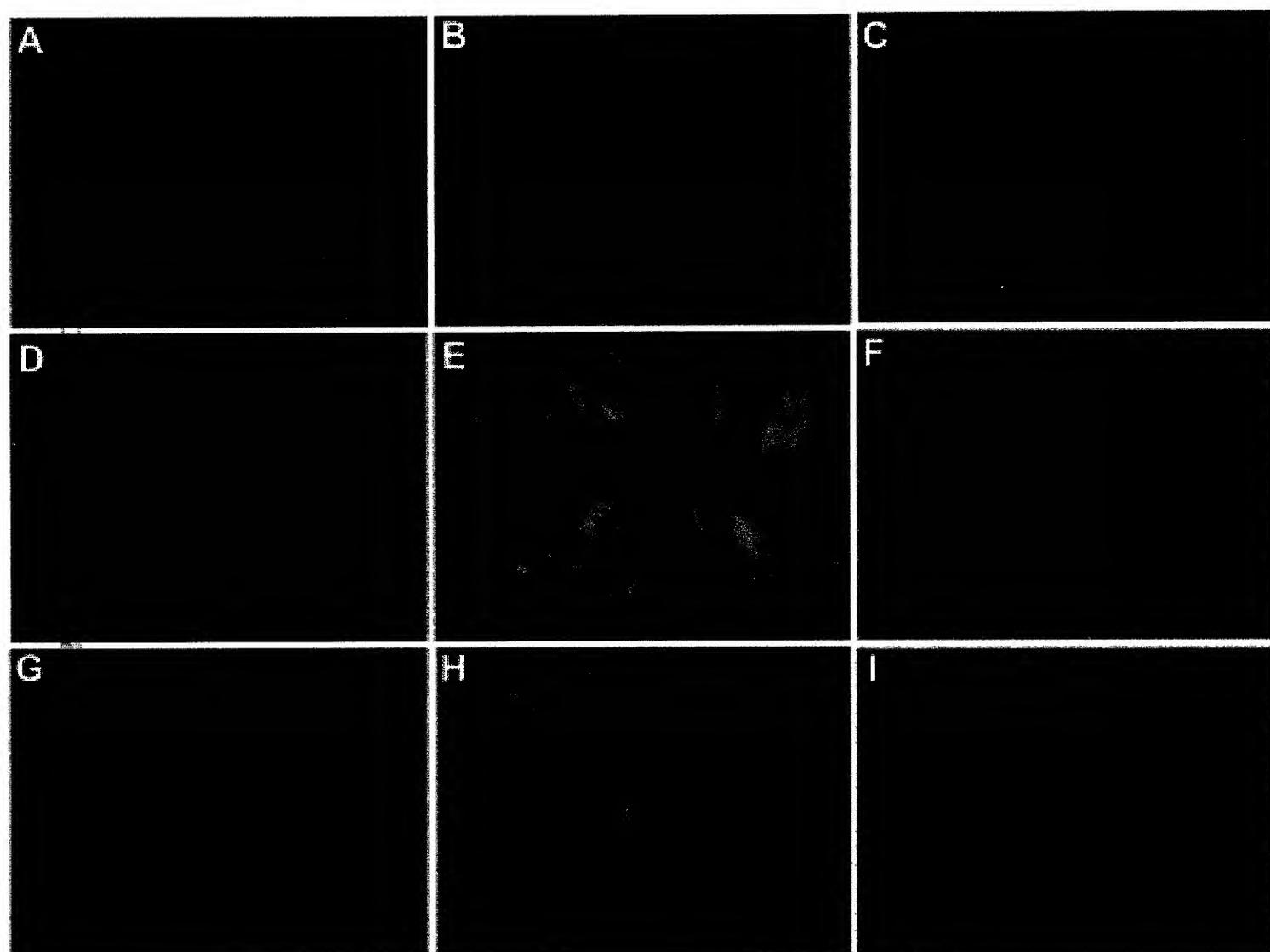


Figure 9  
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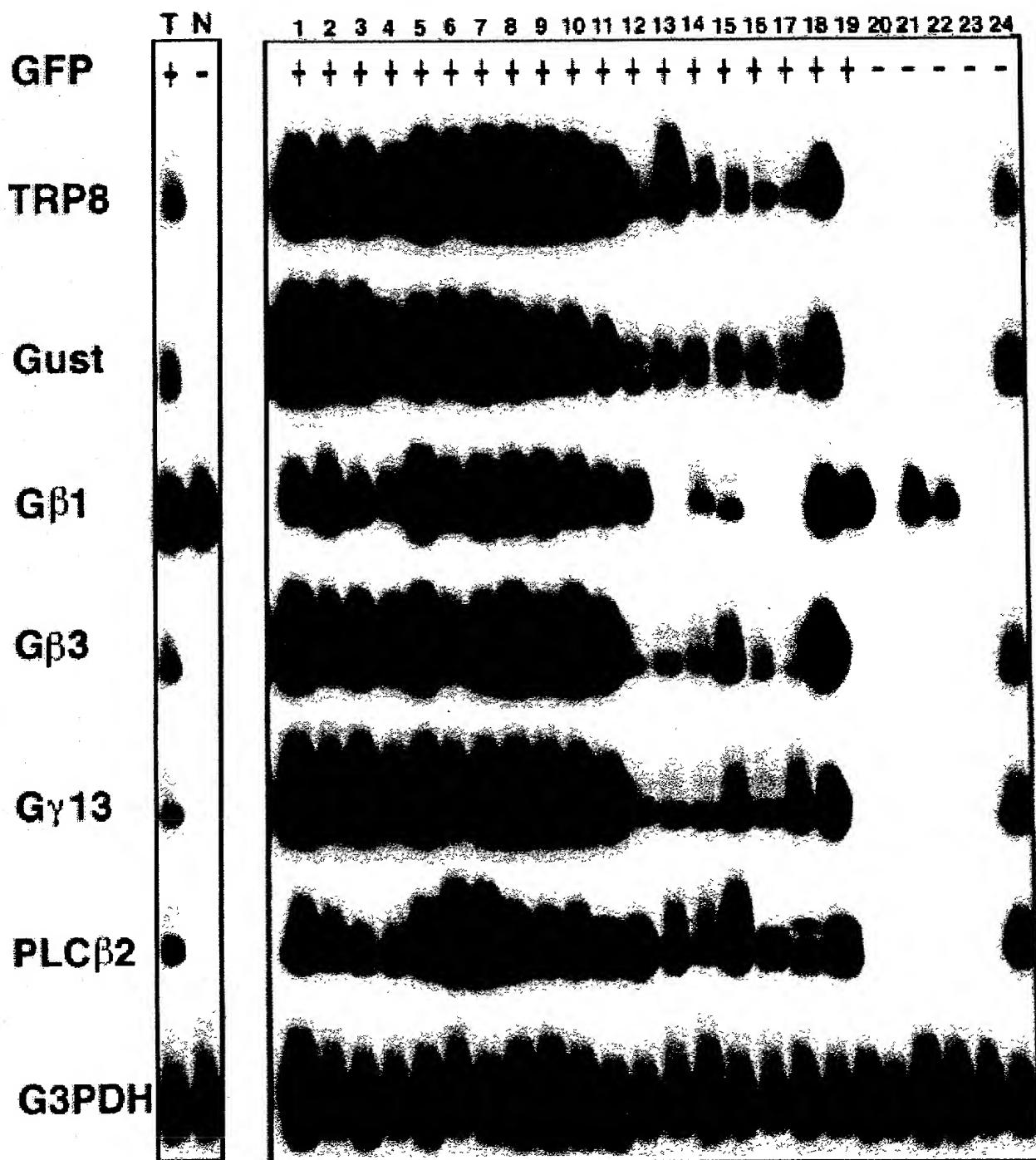


Figure 10  
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Taste  
Brain  
Trp1 260  
Trp2 260  
Trp3 260

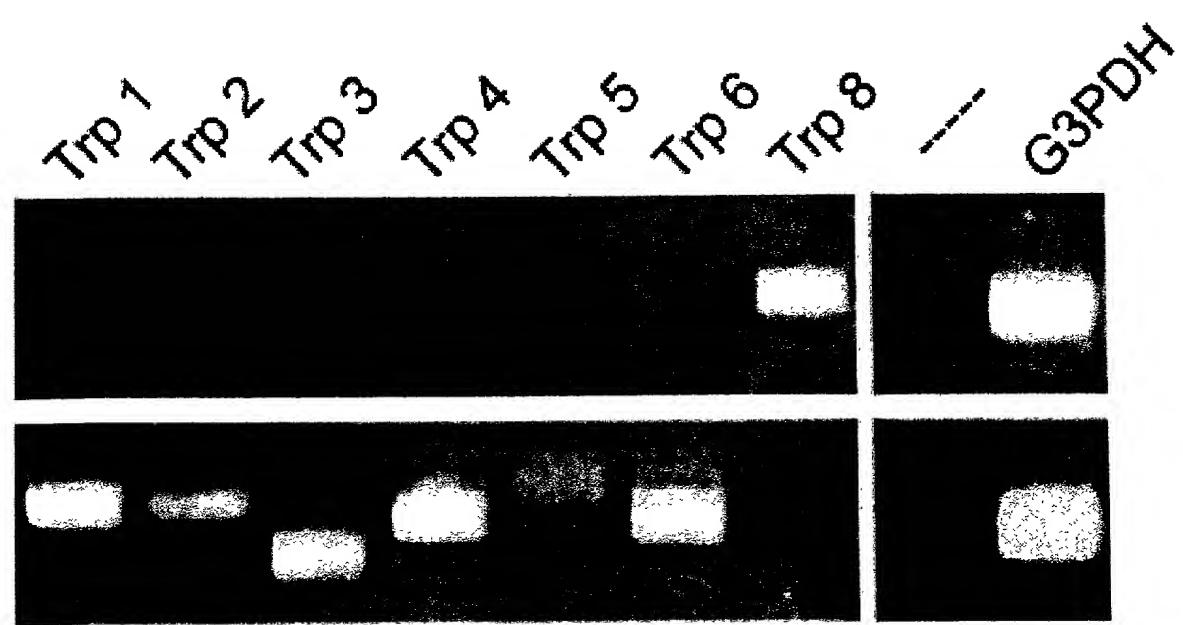
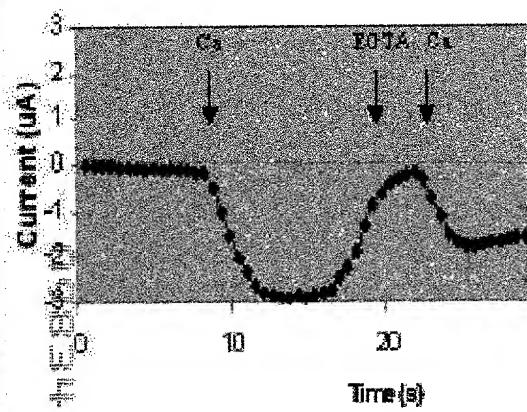
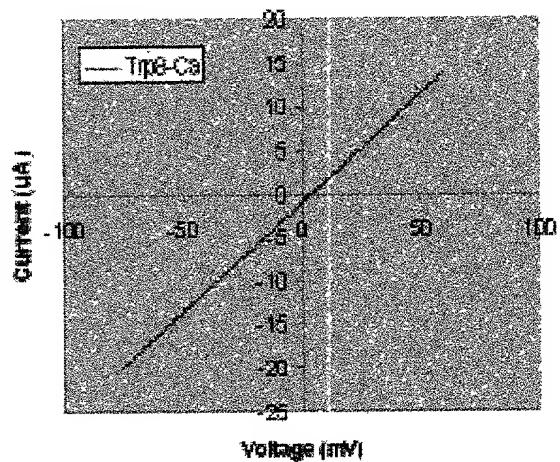


Figure 11  
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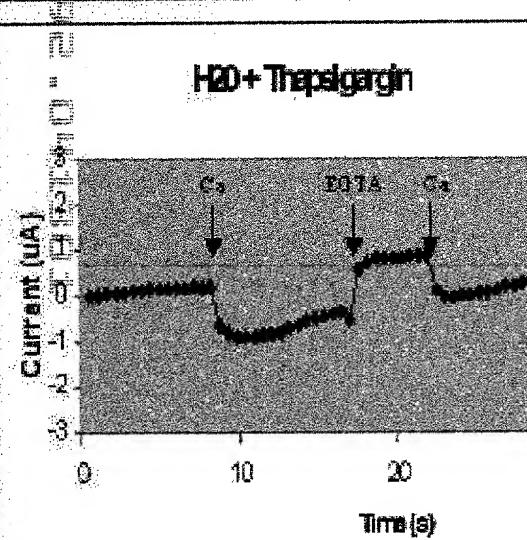
Trp8+Thapsigargin



IV Relationship in Trp8 Injected oocytes



H2O+Thapsigargin



Peak<sub>Max</sub>

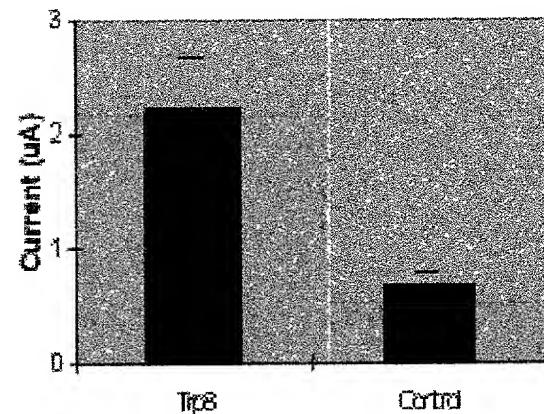
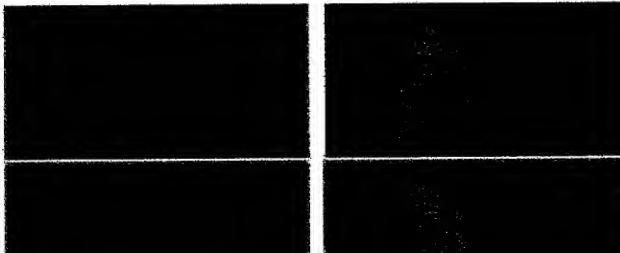


Figure 12  
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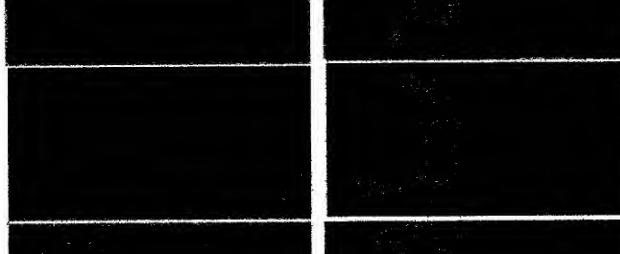
Injected with: **H<sub>2</sub>O**      **TRP8 cRNA**

Thapsigargin 2uM:    +      -      +      -

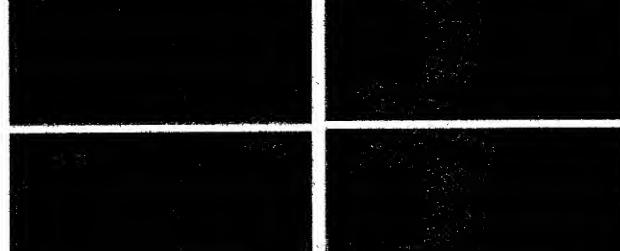
0 s after Ca addition



25 s after Ca addition



50 s after Ca addition



75 s after Ca addition

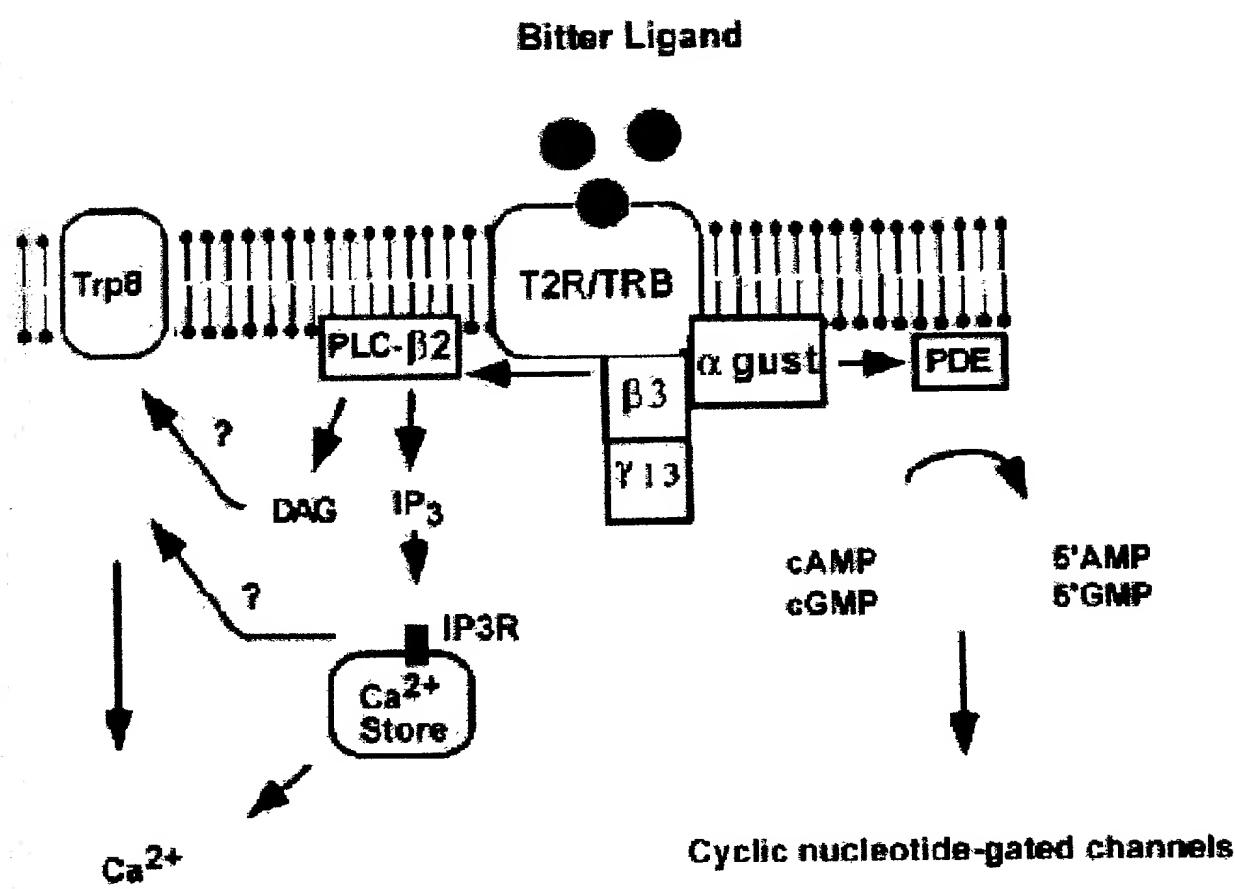


100 s after Ca addition



Figure 13  
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## Transduction of Taste Stimuli



Modified from Kinnamon. *Neuron* (2000) 25:507-510

Figure 14  
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